```
==============================================================
Sequence Listing was accepted with existing errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: Wed Jun 06 09:21:07 EDT 2007
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Application No: 10586312   Version No: 1.0

Input Set:

Output Set:

Started:	2007-05-18 17:03:25.456
Finished:	2007-05-18 17:03:27.180
Elapsed:	0 hr(s) 0 min(s) 1 sec(s) 724 ms
Total Warnings:	32
Total Errors:	64
No. of SeqIDs Defined:	56
Actual SeqID Count:	56

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
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W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna

```
            Input Set:


           Output Set:



             Started:   2007-05-18 17:03:25.456
            Finished:   2007-05-18 17:03:27.180
             Elapsed:   0 hr(s) 0 min(s) 1 sec(s) 724 ms
      Total Warnings:   32
        Total Errors:   64
  No. of SeqIDs Defined: 56
  Actual SeqID Count:    56
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Error code	Error Description
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna

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E  336      Empty lines found between the proteins and the dna
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W  213      Artificial or Unknown found in <213>  in SEQ ID (24)

W  213      Artificial or Unknown found in <213>  in SEQ ID (25)

W  213      Artificial or Unknown found in <213>  in SEQ ID (26)
              This error has occured more than 20 times, will not be displayed
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<110>   Jukka T. SALONEN et al.

<120>   METHOD FOR DETECTING THE RISK OF CARDIOVASCULAR DISEASES SUCH AS ACUTE
        MYOCARDIAL INFARCTION AND CORONARY HEART DISEASE BY ANALYSING DEFENSIN

<130>   0933-0279PUS1

<140>   10586312
<141>   2007-05-18

<150>   US 10/586,312
<151>   2006-07-14

<160>   56

<170>   PatentIn version 3.1

<210>   1
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<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence: PCR primer

<400>   1
cataatttca gcccgatgtg   20

<210>   2
<211>   20
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence: PCR primer

<400>   2
caccctaacc ccctacttct   20

<210>   3
<211>   18
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence: PCR primer

<400>   3
gggcttgctc tttctttc   18

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<210>   4
<211>   18
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence: PCR primer

<400>   4
tccttggttc ctctcatc                                                    18


<210>   5
<211>   18
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence: PCR primer

<400>   5
ctgagtgtgc aggacgag                                                    18


<210>   6
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<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence: PCR primer

<400>   6
cacattgcca aacacgat                                                    18


<210>   7
<211>   736
<212>   DNA
<213>   Homo sapiens

<400>   7
agaaagagga gcatcaaagg gatcttgaga acaaaggcag tccttcccct cccaatcaca      60

tgcccacctc ctctcactgc agcttctgtc tcaggtcttc tcccagcaga gctataaatc     120

caggctgact cctcactccc cacatatcca ctcctgctct ccctcctgca ggtgacccca     180

gccatgagga ccatcgccat ccttgctgcc attctcctgg tggccctgca ggcccaggct     240

gagtcactcc aggaaagagc tgatgaggct acaacccaga agcagtctgg ggaagacaac     300

caggaccttg ctatctcctt tgcaggaaat ggactctctg ctcttagaac ctcaggtagg     360

agacatcaat cttgcacatc tgcaaaatct agaaaaaaag gattggagaa aggatctgga     420

gtcaagtgtg gaaaggtcta cctcacttga gtgactttac ttaatcttcc tggaccttga     480
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ttttctcatc tataaattaa tcagtgagaa ccaaataaat ctaaaagatt ttcttttttc   540

taagactttc agttccaaga tatttctgtg aaatttgcta cttttaagat agaaagacct   600

acactgacta gttctttgta gatctaaatg ggcagactta gttatataga gagtgtttta   660

ctttgtccat tggaaaagct tttagaacct agagaggaac ctataggtgt gttttgatgt   720

aggctaatag gcttga   736

<210> 8
<211> 736
<212> DNA
<213> Homo sapiens

<400> 8
agaaagagga gcatcaaagg gatcttgaga acaaaggcag tccttcccct cccaatcaca   60

tgcccacctc ctctcactgc agcttctgtc tcaggtcttc tcccagcaga gctataaatc   120

caggctgact cctcactccc cacatatcca ctcctgctct ccctcctgca ggtgacccca   180

gccatgagga ccatcgccat ccttgctgcc attctcctgg tggccctgca ggcccaggct   240

gagtcactcc aggaaagagc tgatgaggct acaacccaga agcagtctgg ggaagacaac   300

caggaccttg ctatctcctt tgcaggaaat ggactctctg ctcttagaac ctcaggtagg   360

agacatcaat cttgcacatc tgcaaaatct agaaaaaaag gattggagaa aggatctgga   420

gtcaagtgtg gaaaggtcta cctcacttga gtgactttac ttaatcttcc tggaccttga   480

ttttctcatc tataaattaa tcagtgagaa ccaaataaat ctaaaagatt ttcttttttc   540

taagactttc agctccaaga tatttctgtg aaatttgcta cttttaagat agaaagagct   600

acactgacta gttctttgta gatctaaatg ggcagactta gttatataga gagtgtttta   660

ctttgtccat tggaaaagct tttagaacct agagaggaac ctataggtgt gttttgatgt   720

aggctaatag gcttga   736

<210> 9
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 9
agaaagagga gcatcaaag   19

<210> 10
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 10
tcaagcctat tagcctaca   19

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 11
gacaacctca atgctctgct   20

<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 12
tgacttacct ggacatggct   20

<210> 13
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Snapshot primer

<400> 13
ttttttttttt tttttctttt ttctaagact ttcag   35

<210> 14
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Snapshot primer

<400> 14

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tttttttttt tttttttttg ctacttttaa gatagaaaga                      40


<210>   15
<211>   45
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Snapshot primer

<400>   15
tttttttttt tttttttttt tttttttagt gctgcaagtg agctg                45


<210>   16
<211>   50
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Snapshot primer

<400>   16
tttttttttt tttttttttt tttttttttt tttccagaga ggaagccttg           50


<210>   17
<211>   55
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Snapshot primer

<400>   17
tttttttttt tttttttttt tttttttttt tttttttttc ttgctggcac ccaat     55


<210>   18
<211>   60
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Snapshot primer

<400>   18
tttttttttt tttttttttt tttttttttt tttttttttt tttaccacga cgtcacgcag   60


<210>   19
<211>   30
<212>   DNA
<213>   Artificial Sequence

<220>
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<400> 19
tttttttttt tttgaagacc agccagtgca   30

<210> 20
<211> 1344
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1344)
<223> Coding sequence for variant human ADRA2B gene

<400> 20
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atg gac cac cag gac ccc tac tcc gtg cag gcc aca gcg gcc ata gcg        48
Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala
1               5                   10                  15

gcg gcc atc acc ttc ctc att ctc ttt acc atc ttc ggc aac gct ctg        96
Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
            20                  25                  30

gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac       144
Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
        35                  40                  45

ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc       192
Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
    50                  55                  60

atc atc cct ttc tcg ctg gcc aac gag ctg ctg ggc tac tgg tac ttc       240
Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
65                  70                  75                  80

cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc       288
Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
                85                  90                  95

acc tcg tcc atc gtg cac ctg tgc gcc atc agc ctg gac cgc tac tgg       336
Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
            100                 105                 110

gcc gtg agc cgc gcg ctg gag tac aac tcc aag cgc acc ccg cgc cgc       384
Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
        115                 120                 125

atc aag tgc atc atc ctc act gtg tgg ctc atc gcc gcc gtc atc tcg       432
Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
    130                 135                 140

ctg ccg ccc ctc atc tac aag ggc gac cag ggc ccc cag ccg cgc ggg       480
Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
145                 150                 155                 160
```

```
cgc ccc cag tgc aag ctc aac cag gag gcc tgg tac atc ctg gcc tcc        528
Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
            165                 170                 175

agc atc gga tct ttc ttt gct cct tgc ctc atc atg atc ctt gtc tac        576
Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
            180                 185                 190

ctg cgc atc tac ctg atc gcc aaa cgc agc aac cgc aga ggt ccc agg        624
Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
        195                 200                 205

gcc aag ggg ggg cct ggg cag ggt gag tcc aag cag ccc cga ccc gac        672
Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
    210                 215                 220

cat ggt ggg gct ttg gcc tca gcc aaa ctg cca gcc ctg gcc tct gtg        720
His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
225                 230                 235                 240

gct tct gcc aga gag gtc aac gga cac tcg aag tcc act ggg gag aag        768
Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
                245                 250                 255

gag gag ggg gag acc cct gaa gat act ggg acc cgg gcc ttg cca ccc        816
Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
            260                 265                 270

agt tgg gct gcc ctt ccc aac tca ggc cag ggc cag aag gag ggt gtt        864
Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
        275                 280                 285

tgt ggg gca tct cca gag gat gaa gct gaa gag gag gaa gag gag gag        912
Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu
        290                 295                 300

gag gag tgt gaa ccc cag gca gtg cca gtg tct ccg gcc tca gct tgc        960
Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys
305                 310                 315                 320

agc ccc ccg ctg cag cag cca cag ggc tcc cgg gtg ctg gcc acc cta       1008
Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu
                325                 330                 335

cgt ggc cag gtg ctc ctg ggc agg ggc gtg ggt gct ata ggt ggg cag       1056
Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln
            340                 345                 350

tgg tgg cgt cga agg gcg cac gtg acc cgg gag aag cgc ttc acc ttc       1104
Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg Phe Thr Phe
            355                 360                 365

gtg ctg gct gtg gtc att ggc gtt ttt gtg ctc tgc tgg ttc ccc ttc       1152
Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe
        370                 375                 380

ttc ttc agc tac agc ctg ggc gcc atc tgc ccg aag cac tgc aag gtg       1200
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```
Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val
385                 390                 395                 400


ccc cat ggc ctc ttc cag ttc ttc ttc tgg atc ggc tac tgc aac agc        1248
Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser
                405                 410                 415


tca ctg aac cct gtt atc tac acc atc ttc aac cag gac ttc cgc cgt        1296
Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg
                420                 425                 430


gcc ttc cgg agg atc ctg tgc cgc ccg tgg acc cag acg gcc tgg tga        1344
Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr Ala Trp
        435                 440                 445
```

```
<210>   21
<211>   447
<212>   PRT
<213>   Homo sapiens

<400>   21

Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala
1               5                   10                  15


Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
                20                  25                  30


Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
        35                  40                  45


Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
    50                  55                  60


Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
65                  70                  75                  80


Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
                85                  90                  95


Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
                100                 105                 110


Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
        115                 120                 125


Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
    130                 135                 140
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Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
145   150   155   160

Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
                165   170   175

Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
                180   185   190

Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
        195   200   205

Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
        210   215   220

His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
225   230   235   240

Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
                245   250   255

Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
                260   265   270

Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
        275   280   285

Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu
        290   295   300

Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys
305   310   315   320

Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu
                325   330   335

Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln
                340   345   350

Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg Phe Thr Phe
        355   360   365

Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe
    370   375   380

Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val
385   390   395   400

Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser
                405   410   415

Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg
                420   425   430

Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr Ala Trp
        435   440   445

<210>   22
<211>   1353
<212>   DNA
<213>   Homo sapiens

<220>
<221>   CDS
<222>   (1)..(1353)
<223>   Coding sequence for human ADRA2B gene

<400>   22
atg gac cac cag gac ccc tac tcc gtg cag gcc aca gcg gcc ata gcg   48
Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala
1   5   10   15

gcg gcc atc acc ttc ctc att ctc ttt acc atc ttc ggc aac gct ctg   96
Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
                20   25   30

gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac   144
Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
            35   40   45

ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc   192
Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
    50   55   60

atc atc cct ttc tcg ctg gcc aac gag ctg ctg ggc tac tgg tac ttc   240
Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
65   70   75   80

cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc   288
Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
                85   90   95

acc tcg tcc atc gtg